

Bacterial diversity and profile characteristics of urban soils in New York City

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Objectives

- 1) To collect **dynamic soil properties** (DSP) and **microbial community data** down through the profil.
 - **parent materials:**
 - naturally deposited (NDM)
 - human-altered and human-transported (HAHTM)
 - **management of vegetation cover** (woodland, turf,...)
- 2) To determine the **microbial diversity** and **relative species abundance** and **correlate the microbial communities with the profile characteristics and DSPs**



Sampling sites across NYC



Soils formed in naturally deposited materials (NDM)

*Soils formed in human-altered and human-transported materials (HAHTM)

Samplings & Soil Analysis

- October 2013: **4 soils** formed in NDM (e.g. till, outwash) under **woodland or shrubby cover**
- June 2014: **4 soils** formed in HAHTM (e.g. coal ash, construction debris) with **high artifacts (>10%) fill** under **managed** (turf) or **unmanaged** (weed, forest) **vegetation cover**
- **Sampling of each horizon for microbial analysis** (15-mL Falcon tube) and **soil analysis** (1 kg)
- **Soil analyses on fine fraction (< 2 mm)**
 - heavy metals content (P-XRF)
 - pH (1:1 v/v in water) and salts (1:2 v/v in water)
 - carbonates (volumetric method, NF ISO 10693)
 - organic carbon (loss on ignition at 550° C)

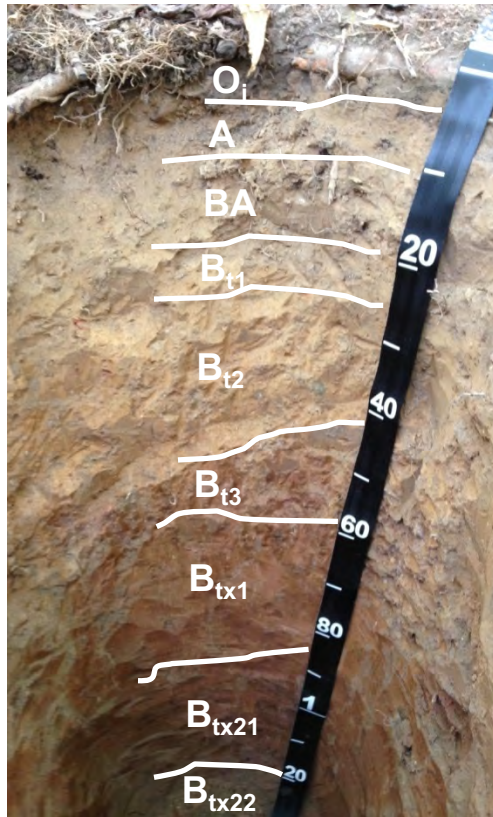


Soil profiles

Haledon

Blue Heron Park,
Staten Island

Parent materials:
glacial till

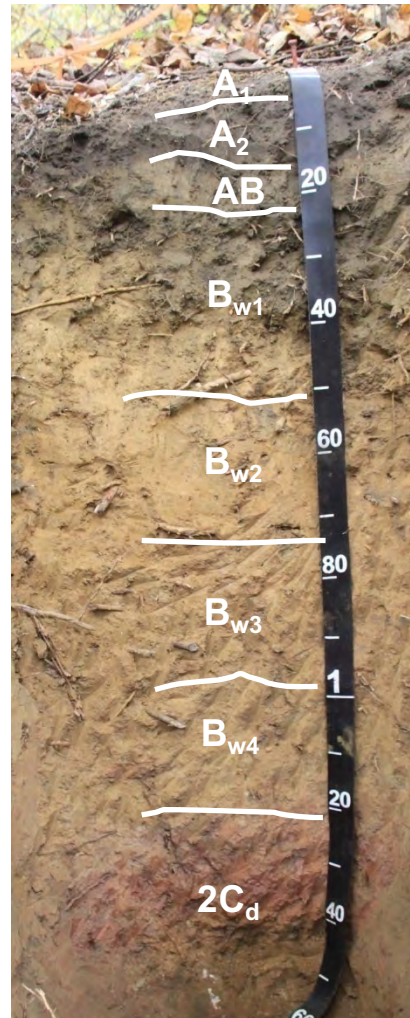


Water table at 42 cm
Fragipan between 57
and 155 cm
Woodland cover

Charlton

Inwood Hill Park,
Manhattan

Parent materials:
eolian deposits over till

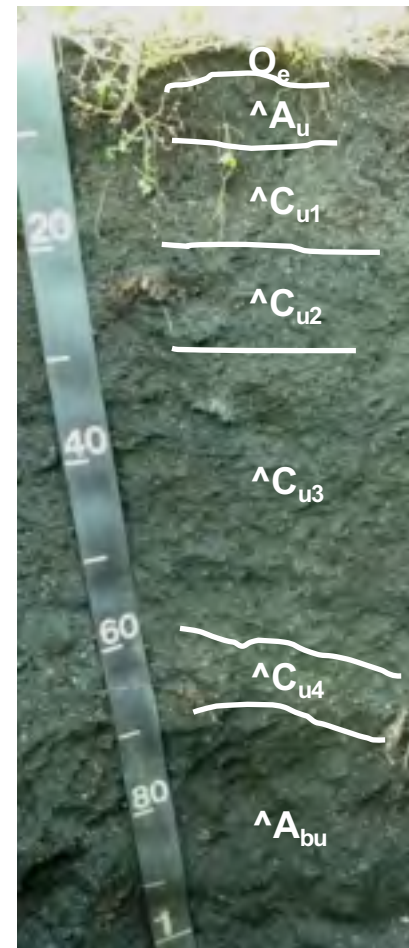


Woodland cover

Rikers

Greenbelt, Staten Island

Parent materials:
coal ash

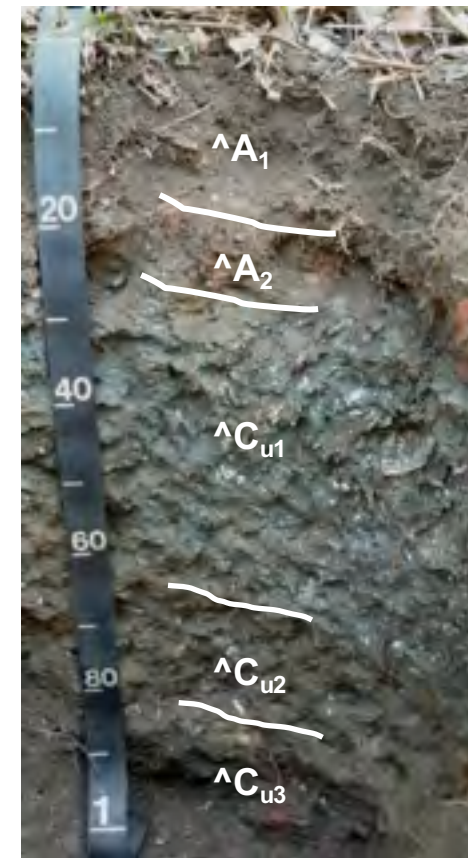


Unmanaged tree cover

Laguardia

Soundview Park, Bronx

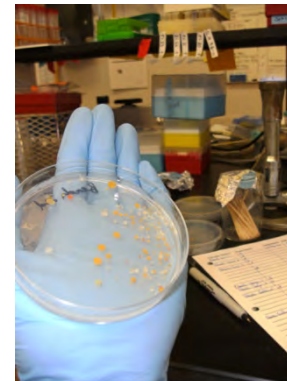
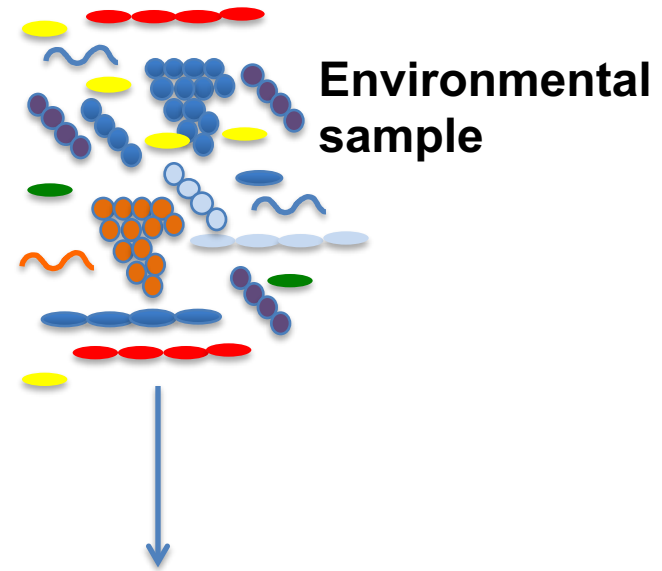
Parent materials:
construction debris



Weed/trees cover

Identifying Soil Microorganisms

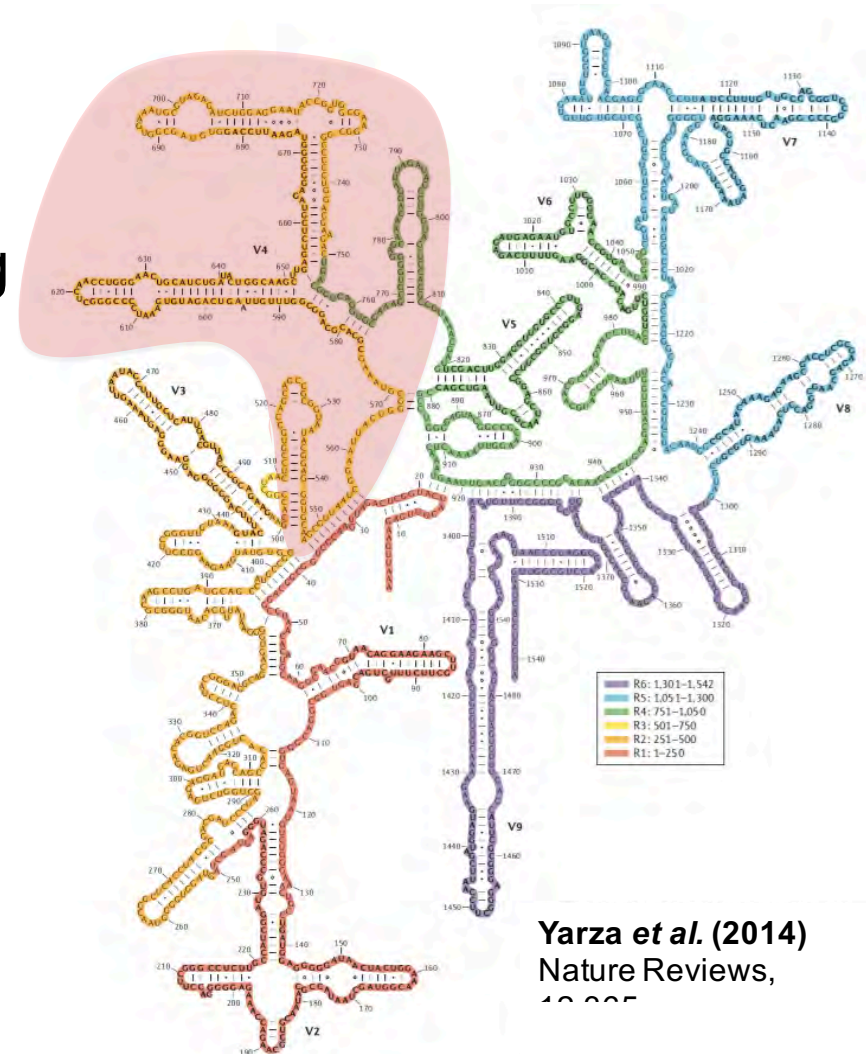
- What is the uncultured majority?
- Complex bacterial communities may contain hundreds or thousands of different bacterial species.
- Typically <5% of this diversity can be cultured in the lab.
- So, how can we learn more about this uncultured majority?



**Culture
in the
lab**

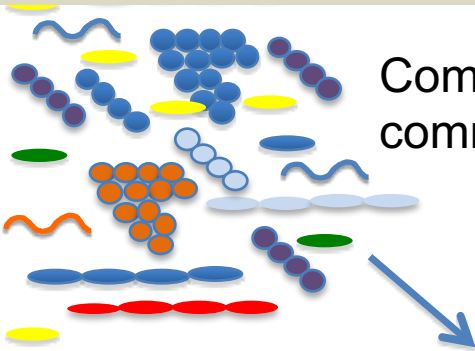
DNA as a proxy for microbial community members

- **DNA sequencing**
- Genomic DNA sequenced using Illumina MiSeq technology
- 16S rRNA gene
 - Variable regions (V1-V3/V4)
- Paired reads



Yarza et al. (2014)
Nature Reviews,
10, 335

Microbiome Analysis Pipeline



Complex soil bacterial community

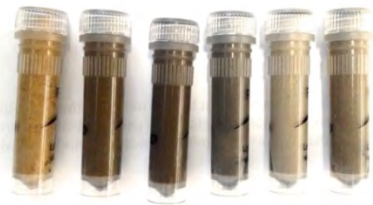
Collect sample and extract DNA



Next generation
Illumina MiSeq
sequencing of DNA



Hundreds of
thousands of DNA
sequence reads



Obtaining DNA



- PowerSoil® DNA isolation kit (MO BIO)
- 0.250 g of soil sample per horizon

Microbiome Analysis Pipeline (2)

Hundreds of
thousands of DNA
sequence reads

AGGCTT → 8
ATTGAA → 1
CGGTAA → 28
TTAAAC → 5

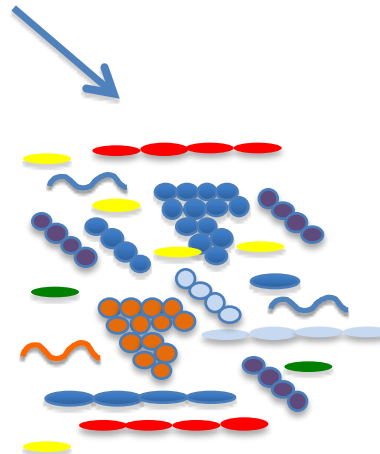
Cluster/bin similar sequences
(>97% identity)
Relative abundance
QIIME software

Compare DNA sequences to
bacterial sequence database

BLAST

Basic Local Alignment Search Tool

DNA sequence information
serves as an indicator for the
presence of organisms,
metabolic pathways, enzymes,
virulence factors, ...



Taxonomic
identification:
Bacillus
Staphylococcus
Clostridium
Streptomyces
Etc...

DNA sequencing and Bioinformatics

- **Bioinformatic pipeline**
- Sequence data processed with QIIME (Quantitative Insights Into Microbial Ecology)
 - Paired sequences
 - Quality control
 - Assignment of operational taxonomic units (OTUs)
 - Identify taxonomy of OTUs
 - Assess biodiversity

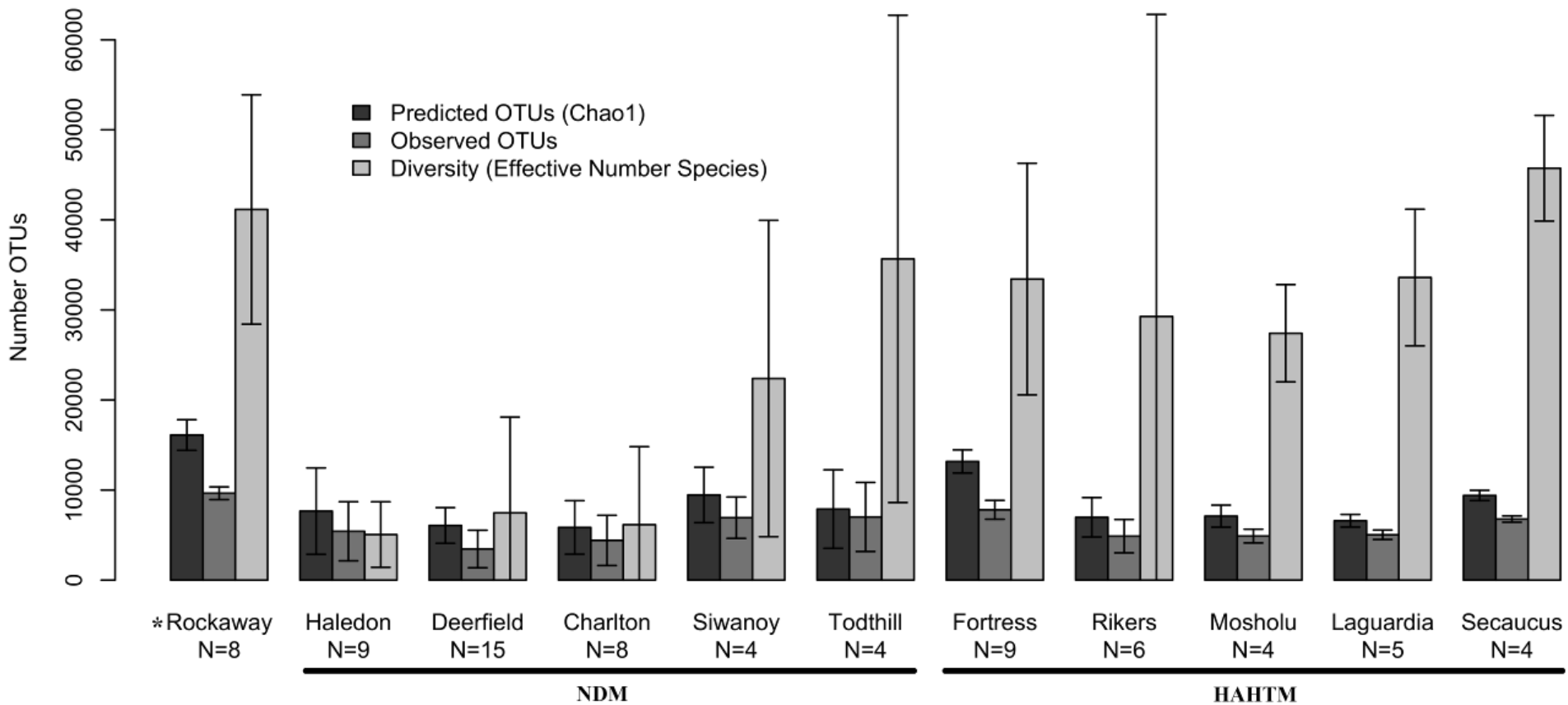


Dynamic Soil Properties

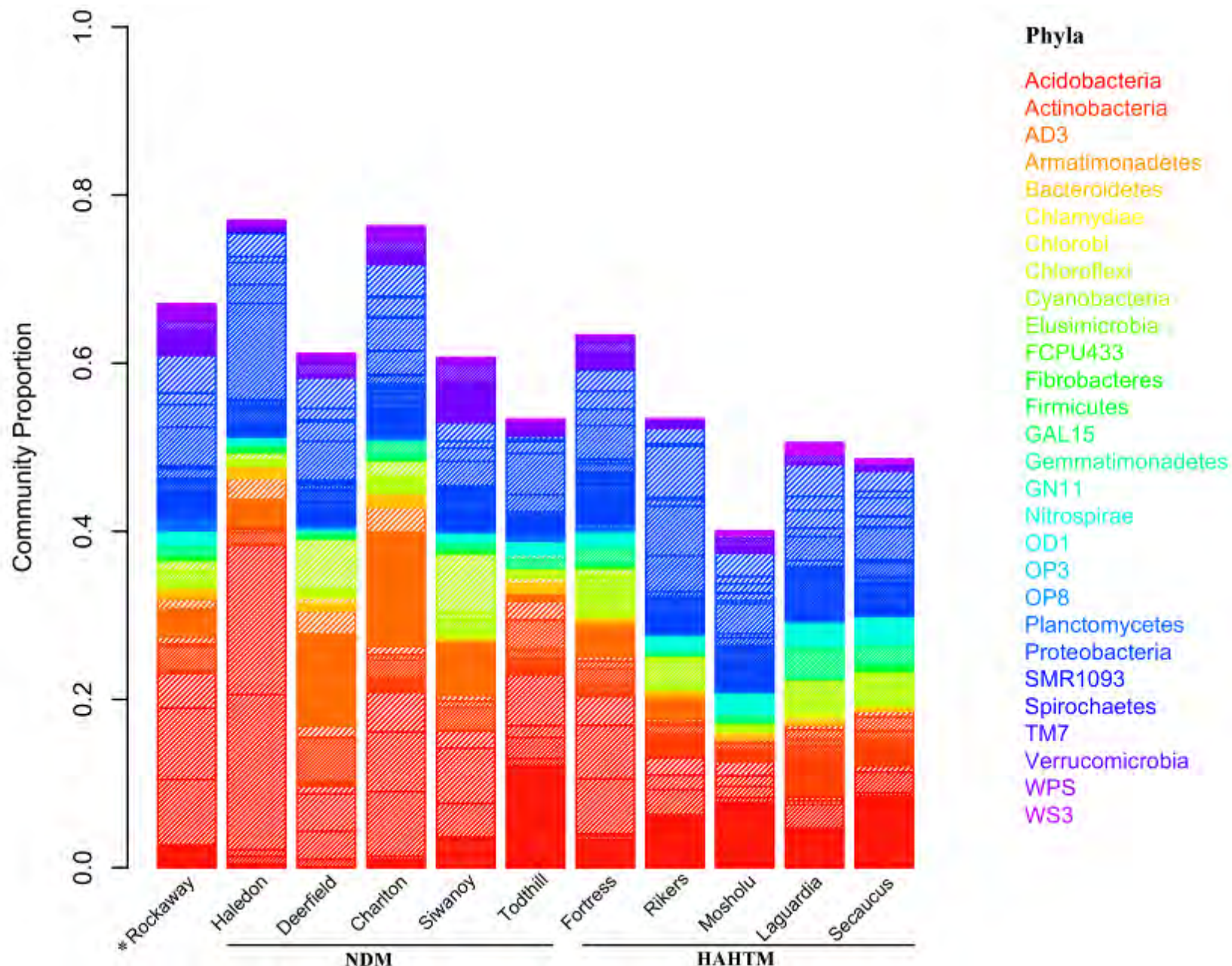
- Higher proportion of **coarse fragments** in soils formed in HAHTM, including a **high proportion of artifacts** (e.g. coal, slag, glass, bricks, concrete)
- **Soils formed in NDM and in coal ash are acidic** whereas **soils formed in construction debris are slightly alkaline**, in relation to the presence of **carbonates** (e.g. concrete)
- **Accumulation of org. C** at the surface is generally higher in NDM soils

	Haledon	Deerfield	Todthill	Charlton	Rikers	Mosholu	Laguardia	Secaucus
parent materials	glacial till	outwash	serpentine	glacial till	coal ash		construction debris	
vegetation	forest	forest	shrub	forest	forest	forest	weed	turf
org. C (%)	1 - 32	0.4 - 42	3 - 16	1.5 - 19	4 - 9	2 – 24	3 - 5	2 - 9
pH (-)	3.5-4.3	3.5-5.3	5.3-6.7	3.7-4.8	4.6-5.1	4.4-6.1	7.0-7.7	6.2-8.2
salts (mg/L)	11-44	21-1010	7-12	17-145	15-80	23-106	102-127	87-165
carbonates (g/kg)	-	-	-	-	-	-	6-33	1-82
coarse fraction (%)	0-7	0	0-45	0-2	35-50	15-75	15-60	0-70

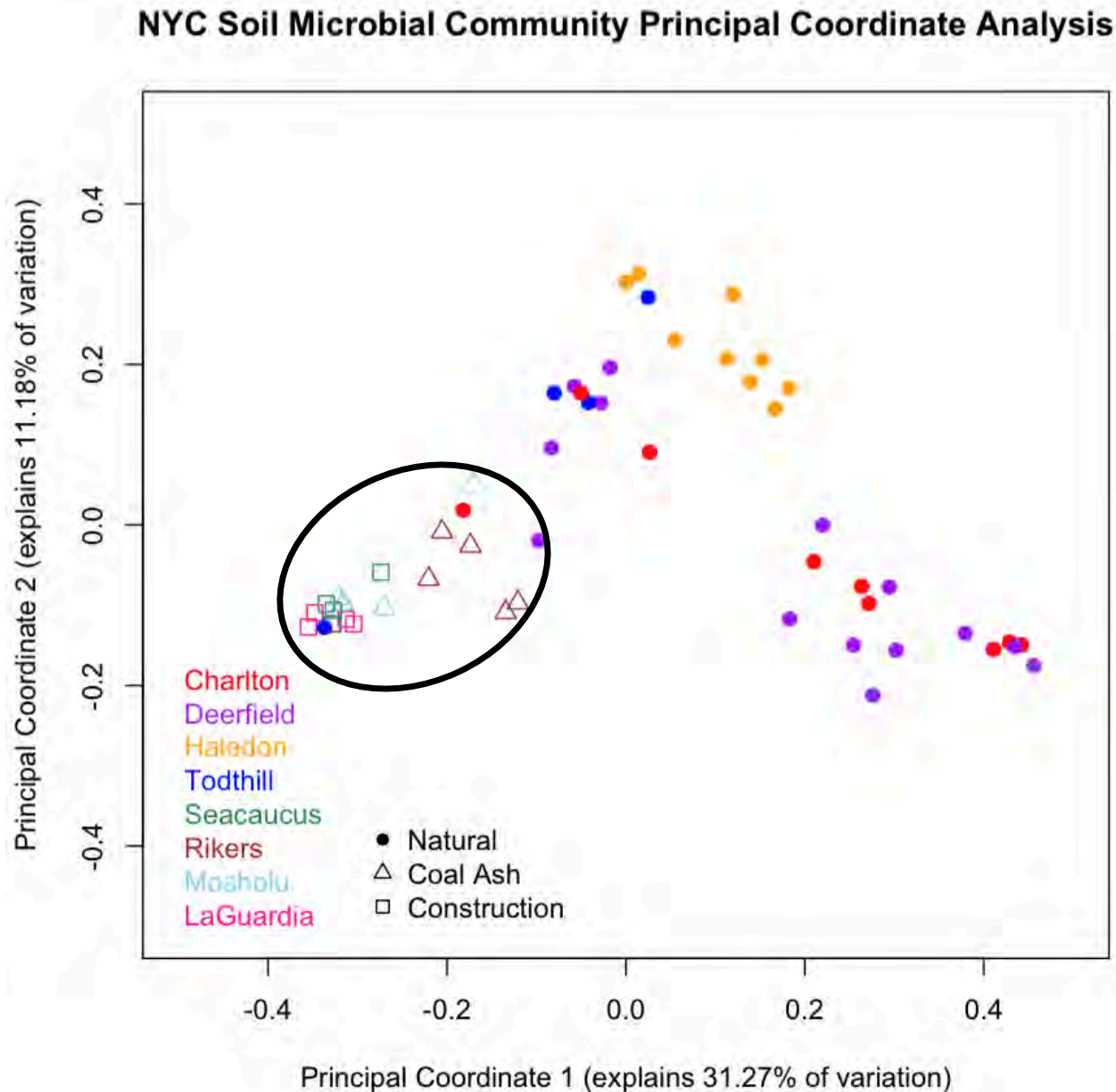
Bacterial Community Biodiversity



Bacterial Community Composition



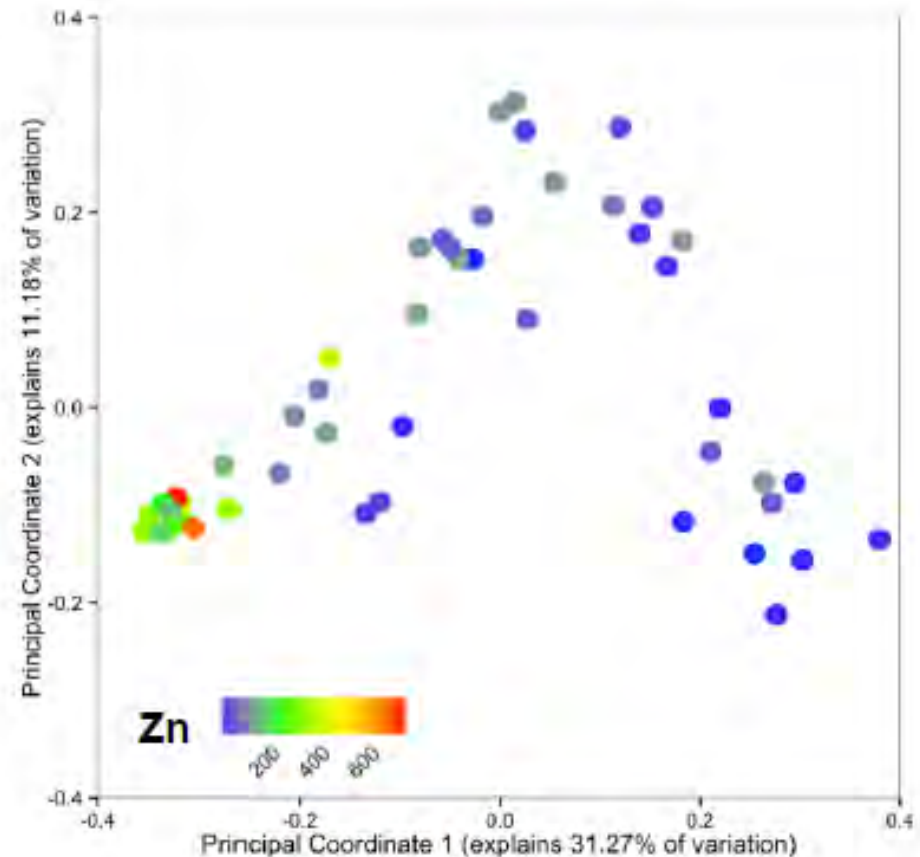
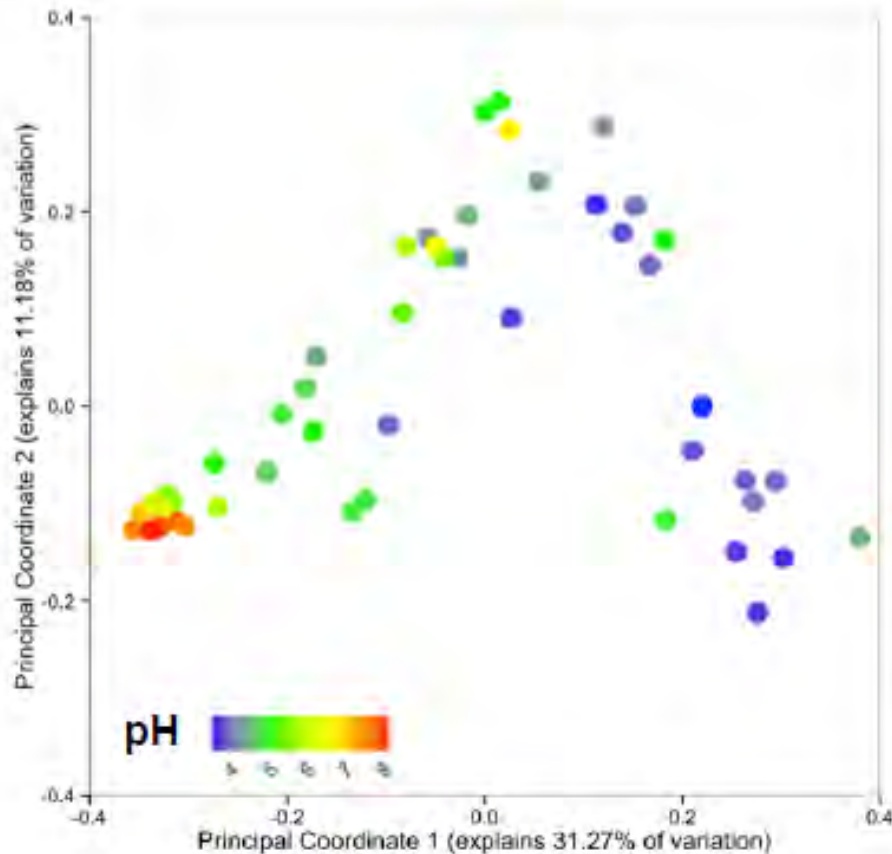
Biodiversity – Bacteria Community Similarities: PCoA



Correlation bacterial diversity and DSPs?

PERMANOVA:

- correlation between diversity and pH ($p=0.006$)
- correlation between diversity and Zn content ($p=0.013$)



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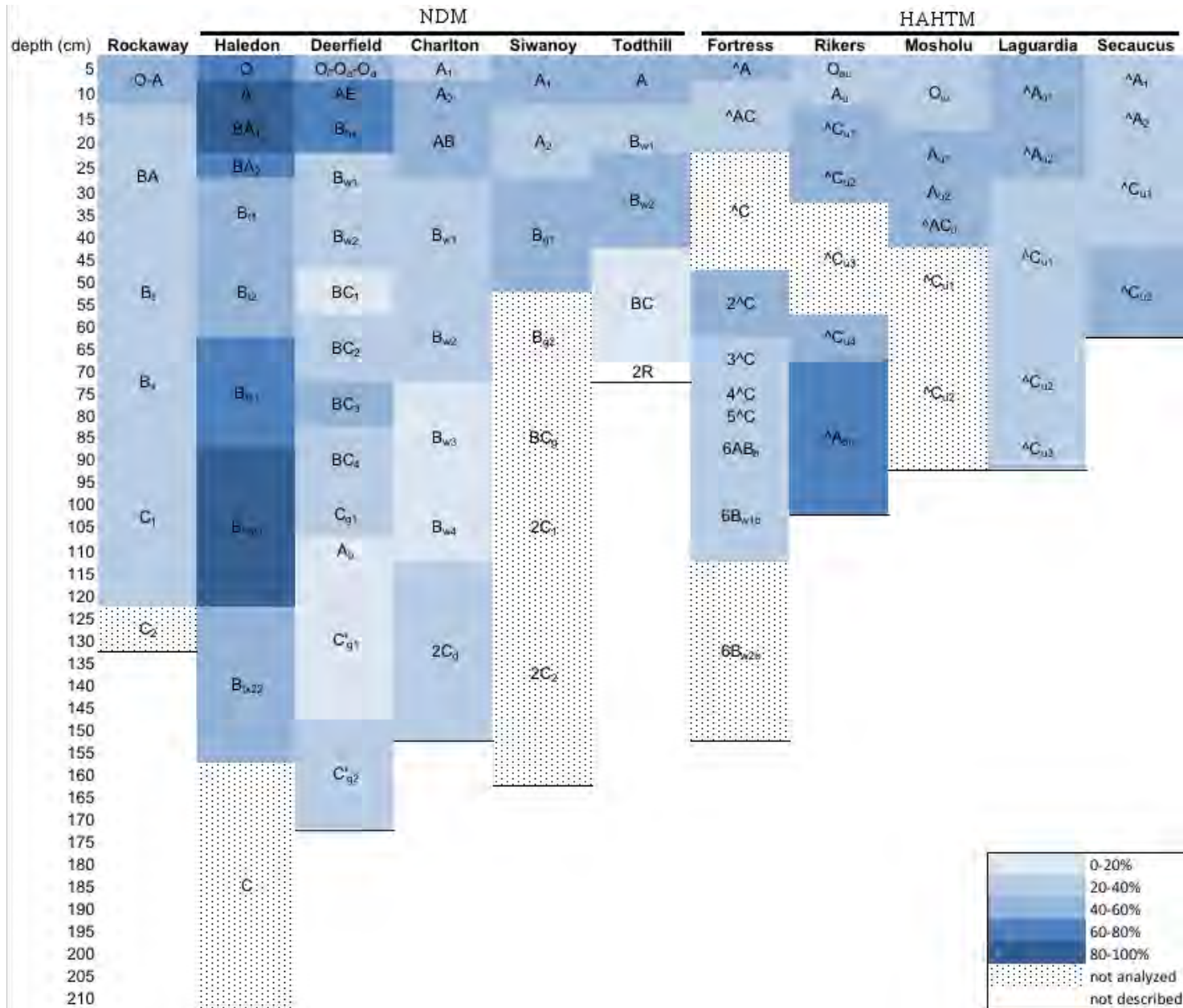
Nadia Brijmohan, Vivian Cheng, Sara Perl Egendorf, Kayo Green, Michael Grinshtein, Xiao Yan Hu, Asia Le, Ying Liu, Tamar Saimbert, Andres Saldarriaga, Kai Saunders, Eridi da Silva, Zulema Su, Sefer Tunca, Susan Valkai, Yuanwei Wang, Zaw Win and Gal Zeidman.



Thank you for your attention

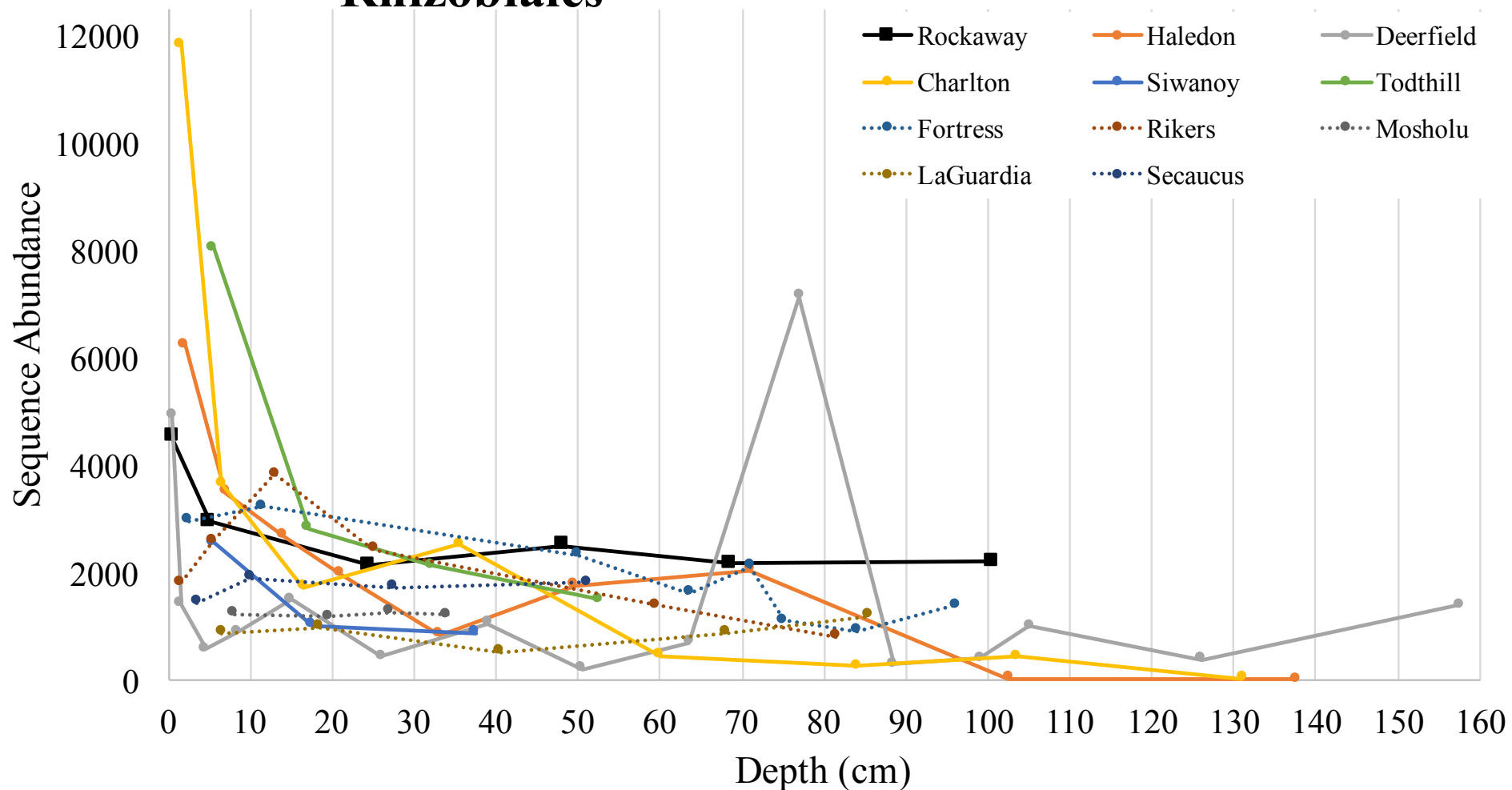


Top Bacteria Presence Through Pedon Depth

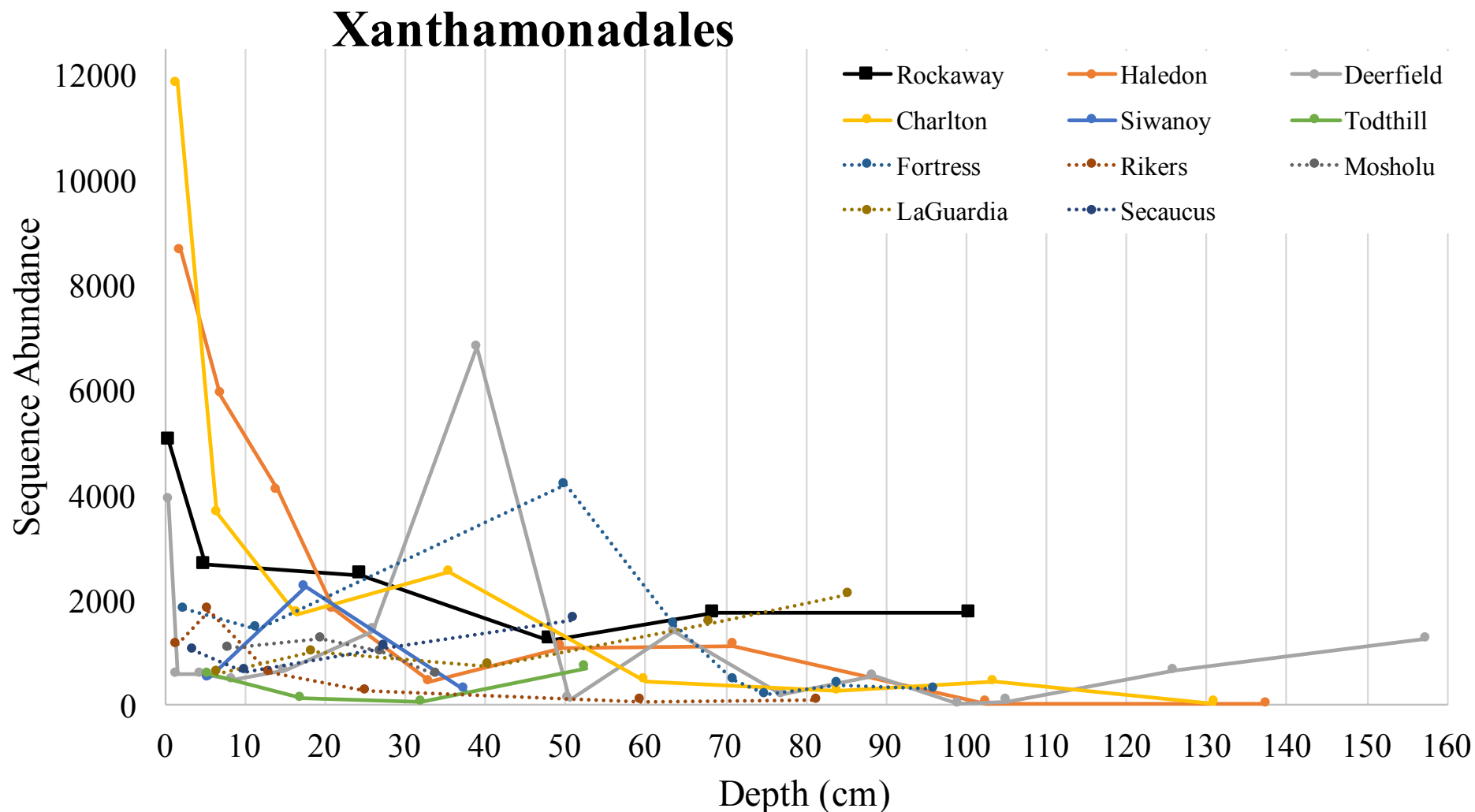


Bacterial Community Composition

Rhizobiales

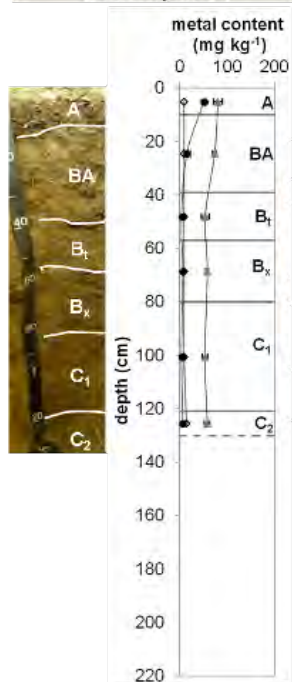


Bacterial Community Composition

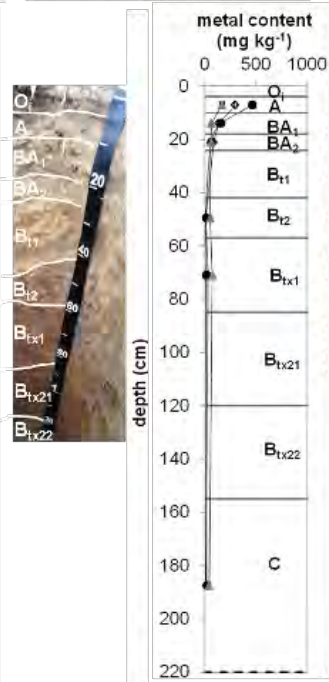


Urban Soil Series Profiles – Natural Parent Material

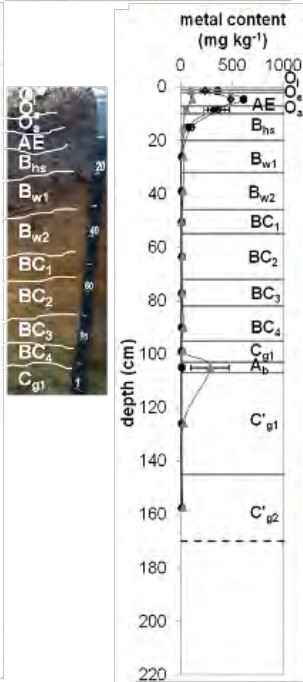
Rockaway series



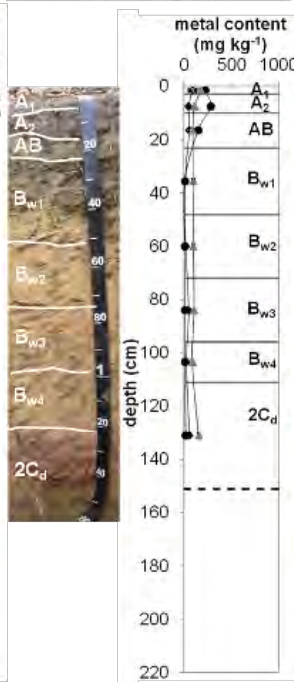
Haledon series



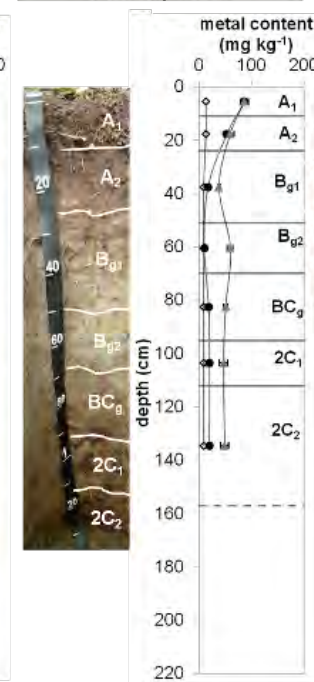
Deerfield series



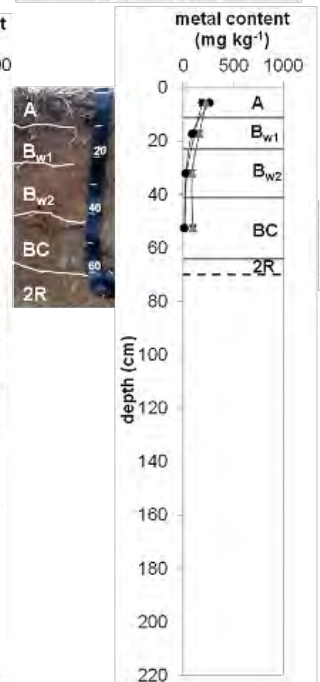
Charlton series



Siwanoy series

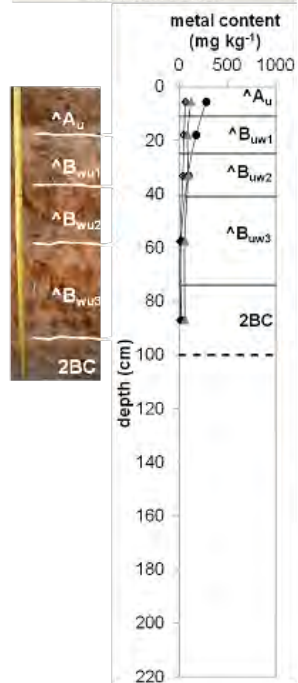


Todthill series

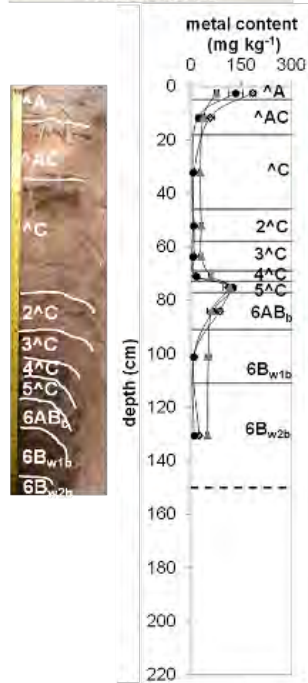


Urban Soil Series Profiles – Anthropogenic Parent Material

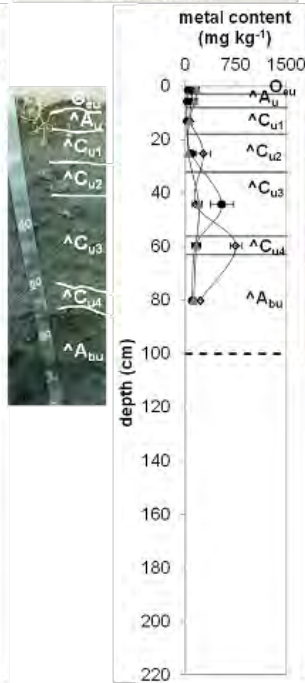
Flatbush series



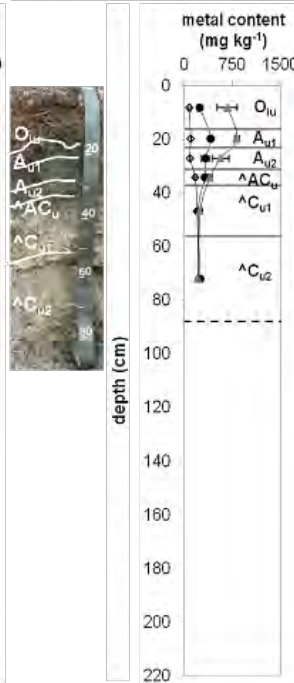
Fortress series



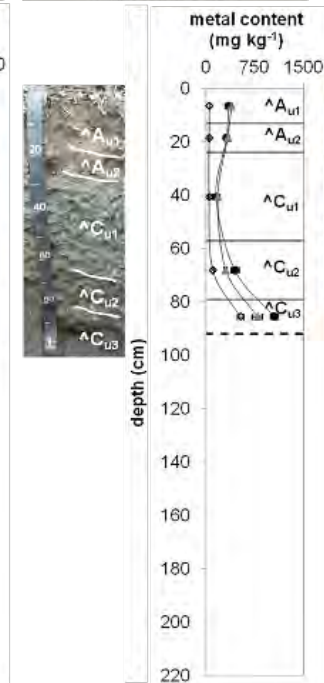
Rikers series



Mosholu series



Laguardia series



Secaucus series

